ATG start codon; amino acids are numbered by assigning +1 to the N-terminal Gln residue after cleavage of the putatuve signal sequence. The N-terminal signal sequence, the region of the active site, and the heme-binding domain are underlined. The numerals I, II and III placed directly above signal nucleotide gaps in the sequence indicate the three intron splice positions. The target site and direction of five different PCR primers are shown with dotted lines above the nucleotide sequence. An asterisk (*) marks the translation stop codon.

Please replace the paragraph beginning at page 9, line 14, with the following rewritten paragraph:

Figures 2A and 2B are the genomic DNA sequence of the Soybean seed coat peroxidase.

Please replace the paragraph beginning at page 9, line 16, with the following rewritten paragraph:

Figures 3A-(1)-3A(4) and 3B are a comparison of soybean seed coat peroxidase with other closely related plant peroxidases. The GenBank accession numbers are provided next to the name of the plant from which the peroxidase was isolated. The accession number for the soybean sequence is L78163. (Fig. 3A-(1)-3A-(4)) A comparison of the nucleic acid sequences; (Fig. 3B) A comparison of the amino acid sequences.

Please replace the paragraph beginning at page 11, line 3, with the following rewritten paragraph:

Figures 7A and 7B exhibit PCR analysis of an F2 population from a cross of *EpEp* and *epep* genotypes. Genomic DNA was used as template for PCR analysis of the parents (P) and 30 F_2 individuals. The cross was derived from the soybean lines OX312 (*epep*) and OX347 (*EpEp*). Plants were self pollinated and seeds were collected and scored for seed coat peroxidase activity. The symbols (-) and (+) indicate low and high seed coat peroxidase activity, respectively. Primers prx9+ and prx10- were used in the amplification reactions. Products were separated by electrophoresis through a 0.8% agarose gel and visualized under UV light after staining with ethidium bromide. The migration of molecular markers and their corresponding size in kb is also shown (lanes M).

Please replace the paragraph beginning at page 11, line 14, with the following rewritten paragraph:

Figures 8A-8C display PCR analysis of six different soybean cultivars with primers derived from the seed coat peroxidase cDNA sequence. Genomic DNA was used as template for PCR analysis of three *EpEp* cultivars and three *epep* cultivars. Primers used in the amplification reactions and the size of the DNA product is indicated on the left. Products were separated by electrophoresis through a 0.8% agarose gel and visualized under UV light after staining with ethidium bromide.

(Fig. 8A) Forward and reverse primers are downstream from deletion

(Fig. 8B) Forward primer anneals to site within deletion

(Fig. 8C) Primers span deletion

Please replace the paragraph beginning at page 12, line 2, with the following rewritten paragraph:

Figures 9A and 9B show the accumulation of peroxidase RNA in tissues of GEp and *epep* plants. **Figure 9(A)**: A comparison of peroxidase transcript abundance in cultivars Harosoy 63 (Ep) or Marathon (ep). Seed and pod tissues were sampled at a late stage of development corresponding to a whole seed fresh weight of 250 mg. Root and leaf tissue was from six week old plants. Autoradiograph exposed for 96 h. **Figure 9(B)**: Developmental expression of peroxidase in cultivar Harosoy 63 (EP). Flowers were sampled immediately after opening. Seed coat tissues were sampled at four stages of development corresponding to a whole seed fresh weight of: lane 1, 50 mg; lane 2, 100 mg; lane 3, 200 mg; lane 4, 250 mg. Autoradiograph exposed for 20 h.

IN THE CLAIMS:

Please substitute the following amended claims for corresponding claims previously presented. A copy of the amended claims showing current revisions is attached.

Amend claims 19-22 as follows: